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AMENDMENTS TO THE SPECIFICATION

Please replace the existing paragraph beginning at page 1, line 6, with the following rewritten paragraph:

--This application is a continuation-in-part of U.S. Application Serial No. 09/649,167 filed August 23, 2000, entitled "Novel Nucleic Acids and Polypeptides," Attorney Docket No. 790CIP (now abandoned) which is a continuation-in-part of U.S. Application Serial No. 09/540,217 filed March 31, 2000, entitled "Novel Nucleic Acids and Polypeptides," Attorney Docket No. 790 (now abandoned); and is a continuation-in-part application of U.S. Application Serial No. 09/684,711 filed October 6, 2000, entitled "Methods and Materials Relating to Alpha-2-Macroglobulin-Like Polypeptides and Polynucleotides," Attorney Docket No. HYS-31 (now abandoned) which is a continuation-in-part of U.S. Application Serial No. 09/560,875 filed April 27, 2000, entitled "Novel Nucleic Acids and Polypeptides," Attorney Docket No. 787CIP (now abandoned) which is a continuation in part of U.S. Application Serial No. 09/496,914 filed February 03, 2000, entitled "Novel Contigs Obtained from Various Libraries," Attorney Docket No. 787 (now abandoned); all of which are incorporated herein by reference in their entirety.--

Please replace the existing paragraph beginning at page 12, line 12, with the following rewritten paragraph:

-- Complement component C3d homologous sequence

LQNLDGLVQMPSGCGEQNMVLFAPIIYVLQYLEKAGLLTEEIRSRAVGFLEIGYQKELM
YKHSNGSYSAFGERDGNGNTWLTAFVTKCFGQAQKFIFIDPKNIQDALKWMAGNQLPS
GCYANVGNLLHTAMKGGVDDEVSLTAYVTAALLEMGKDVDDPMVSQGLRCLKNSAT
STTNLYTQALLAYIFSLAGEMDIRNILLKQLDQQAIISGESIYWSQKPTPSSNASPWSEPA
AVDVELTAYALLAQLTKPSLTQKEIAKATSIVAWLAKQHNAYGGFSSTQDTVVALQAL
AKYATTAY

(designated as SEQ ID NO: 21) with PSI-BLAST e-value of 4.4e-87, protein database identification number entry = 1c3d ([Research collaboratory for Structural Bioinformatics.

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~~http://www.resb.org/pbd~~Berman et al., Nucl. Acids Res. 28:235-242 (2000)], verify score = 0.49, located at residues 977-1276 of SEQ ID NO: 4.--

Please replace the existing paragraph beginning at page 13, line 5, with the following rewritten paragraph:

--Receptor domain alpha-2-macroglobulin domain

NMKTFSLSVEIGKARCEQPTSPRSLTLTIHTSYVGSRSSSNMAIVEVKMLSGFSPM EGTNQLLLQQPLVKKVEFGTDTLNIYLDELIKNTQTYTFTISQSVLVTNLKPATIKVYDY YLPGSFKLSQYTIVWSMNNDS

(designated as SEQ ID NO: 22) with PSI-BLAST e-value of 4.4e-52, protein database identification number entry = 1bv8 {[Research collaboratory for Structural Bioinformatics. ~~http://www.resb.org/pbd~~Berman et al., Nucl. Acids Res. 28:235-242 (2000)), verify score = 0.49, located at residues 1349-1479 of SEQ ID NO: 4.--

Please replace the existing paragraph beginning at page 130, line 5, with the following rewritten paragraph:

--Polypeptides were predicted to be encoded by SEQ ID NO: 2 and SEQ ID NO: 27 as set forth below. The polypeptide was predicted using a software program called FASTY (~~available from http://fasta.bioch.virginia.edu~~University of Virginia) which selects a polypeptide based on a comparison of translated novel polynucleotide to known polypeptides (W.R. Pearson, Methods in Enzymology, 183: 63-98 (1990), herein incorporated by reference).--

Please replace the existing paragraph beginning at page 134, line 12, with the following rewritten paragraph:

-- Complement component C3d homologous sequence

LQNLDGLVQMPSGCGEQNMVLFAPIIYVLQYLEKAGLLTEEIRSRAVGFLEIGYQKELM YKHSNGSYSAFGERDGNGNTWLTAFVTKCFGQAQKFIFIDPKNIQDALKWMAGNQLPS GCYANVGNLLHTAMKGGVDDEVSLTAYVTAALLEMGKDVDDPMVSQGLRCLKNSAT

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STTNLYTQALLAYIFSLAGEMDIRNILLKQLDQQAIISGESIYWSQKPTPSSNASPWSEPA
AVDVELTAYALLAQLTKPSLTQKEIAKATSIVAWLAKQHNAYGGFSSTQDTVVALQAL
AKYATTAY

(designated as SEQ ID NO: 21) with PSI-BLAST e-value of 4.4e-87, protein database
identification number entry = 1c3d ([Research collaboratory for Structural Bioinformatics.
http://ww.rcsb.org/pbdBerman et al., Nucl. Acids Res. 28:235-242 (2000)], verify score = 0.49,
located at residues 977-1276 of SEQ ID NO: 4.--

Please replace the existing paragraph beginning at page 135, line 8, with the following rewritten
paragraph:

--Receptor domain alpha-2-macroglobulin domain

NMKTFSLSVEIGKARCEQPTSPRSLTLTIHTSYVGSRSSSNMAIVEVKMLSGFSPM
EGTNQLLLQQPLVKKVEFGTDTLNIYLDELIKNTQTYTFTISQSVLVTNLKPATIKVYDY
YLPGSFKLSQYTIVWSMNNDS
(designated as SEQ ID NO: 22) with PSI-BLAST e-value of 4.4e-52, protein database
identification number entry = 1bv8 ([Research collaboratory for Structural Bioinformatics.
http://ww.rcsb.org/pbdBerman et al., Nucl. Acids Res. 28:235-242 (2000)), verify score = 0.49,
located at residues 1349-1479 of SEQ ID NO: 4.--